

REMARKS/ARGUMENTS***Claim amendments***

Claim 72 is amended. Claims 1, 3-47, 49-60, and 67-71 are cancelled without prejudice or disclaimer. Claims 2, 48, 61-66 and 72 are currently pending.

Claim 72 has been amended to indicate that the modified *Trichoderma reesei* xylanase II comprises an amino acid sequence that is from 93 to 99% identical to SEQ ID NO: 16. Support for this amendment may be found by alignment of the amino acid sequences of xylanase II at are described in Table 2. One skilled in the art of nucleic acid and amino acid sequences routinely calculates such sequence similarities which are herein inherently supported by the discussion and sequences provided in the original disclosure.

Multiple alignment of the amino acid sequences of *Trichoderma reesei* xylanase II (TrX) with each of the modified TrX of the present invention comprising amino acid substitutions at one or more of position 116, 118, 144, and 144 and 161 was conducted using the publicly available ClustalW multiple alignment program (Chenna R., et al., 2003, Nucl. Acids Res. 31: 3497-3500; <http://www.ebi.ac.uk/Tools/clustalw2/index.html>). Alignment of TrX with each of the modified TrX variants, and alignment of each of the variants with each other, resulted in a 93-99% sequence identity to each other. A copy of the results of the ClustalW alignment are attached as Exhibit 1 (Clustalw2—HTX18 pat seqa.txt). Data provided in Figures 3-11 of the present application demonstrate that amino acid substitutions at positions 116, 118, 144, 144, and 161, enhance the thermophilicity and/or alkalophilicity of native TrX2 and also variants of TrX2 that comprise these additional amino acid substitutions.

Rejections under 35 USC §112

Claims 2, 48, 61-66 and 72 are rejected under 35 USC 112 (first paragraph) as failing to comply with the enablement requirement. Examiner states that the specification does not provide enablement for any modified *Trichoderma reesei* xylanase II, and any modification at positions 116, 118, 144 161 or a combination thereof. Applicant respectfully traverses this rejection.

Claims 2, 48 and 61-66 depend from claim 72 and include the limitations of this base claim.

Claim 72 states that the modified *Trichoderma reesei* xylanase II is selected from a group consisting of a defined list of 12 modified *Trichoderma reesei* xylanase II proteins that have been described in the specification and that comprise specified modifications at one or more of positions 116, 118, 144, 161. The claim is therefore not directed to any modified *Trichoderma reesei* xylanase II as suggested by Examiner.

To further clarify claim 72, this claim has been amended to rearrange the wording of this claim.

Removal of the rejection to claims 2, 48, and 61-66 under 35 USC 112 (first paragraph) is respectfully requested.

Claims 2, 48, 61-66 and 72 are also rejected under 35 USC 112 (first paragraph) as failing to comply with the written description requirement. Examiner states that the claims contain subject matter that was not described in the specification. Applicant respectfully disagrees with this rejection.

Claims 2, 48 and 61-66 depend from claim 72 and include the limitations of this base claim.

Claim 72 states that the modified *Trichoderma reesei* xylanase II is selected from a group consisting of a defined list of 12 mutant modified *Trichoderma reesei* xylanase II proteins that have been described in the specification and that comprise specified modifications at positions 116, 118, 144, 161 or a combination thereof. The claim is therefore not directed to any variant of *Trichoderma reesei* xylanase II as argued by Examiner.

Examiner argues that the claimed proteins in claims 2, 48, 61-66 and 72 can have any structure even structures with low percentage of similarity or even no similarity to SEQ ID NO: 16. Applicant has amended claim 72 to indicate that the modified *Trichoderma reesei* xylanase II comprises an amino acid sequence that is from 93 to 99% identical to SEQ ID NO: 16.

Removal of the rejection to claims 2, 48 and 61-66 under 35 USC 112 (first paragraph) is respectfully requested.

It is respectfully submitted that the above-identified application is now in a condition for allowance and favorable reconsideration and prompt allowance of these claims is respectfully requested. Should the Examiner believe that anything further is desirable in order to place the application in better condition for allowance, the Examiner is invited to contact the Applicant's undersigned attorney at the telephone number listed below.

Except for issue fees payable under 37 C.F.R. § 1.18, the Commissioner is hereby authorized by this paper to charge any additional fees during the entire pendency of this application including fees due under 37 C.F.R. §§ 1.16 and 1.17 which may be required, including any required extension of time fees, or credit any overpayment to Deposit Account No. 50-1283.

Atty Docket No.: GOWL-018/00US

Appln. No.: 09/990,874

Dated: July 30, 2008

Respectfully submitted,
COOLEY GODWARD KRONISH LLP

COOLEY GODWARD KRONISH LLP
ATTN: Patent Group
777 6th Street NW, Suite 1100
Washington, DC 20001

By:

Erich E. Veitenheimer
Erich E. Veitenheimer, Ph.D
Reg. No. 40,420

Tel: (202) 842-7800
Fax: (202) 842-7899

EXHIBIT 1

ClustalW2--HTX18 pat seqa.txt

ClustalW2Help
 General Help
 Formats
 Gaps
 Matrix
 References
 ClustalW2 Help
 ClustalW2 FAQ
 Jalview Help
 Scores Table
 Alignment
 Guide Tree
 Colours
 ClustalW2 Results

Results of search
 Number of sequences11
 Alignment score64595
 Sequence formatPearson
 Sequence typeaa
 Jalview
 Output fileclustalw2-20080418-16010091.output
 Alignment fileclustalw2-20080418-16010091.aln
 Guide tree fileclustalw2-20080418-16010091.dnd
 Your input fileclustalw2-20080418-16010091.input

To save a result file right-click the file link in the above table and choose "Save Target As".
 If you cannot see the Jalview button, reload the page and check your browser settings to enable Java Applets.

Scores Table

Alignment Score Sequence Number Sequence Name Sequence Length

SeqA Name	Len(aa)	SeqB Name	Len(aa)	Score
1 TrX	190	2 TrX116G	190	99
1 TrX	190	3 TrX118C	190	99
1 TrX	190	4 TrXHMLAHAE144R	190	95
1 TrX	190	5 TrXHMLAHAE144R161R	190	95
1 TrX	190	6 TrXHMLAHAE116G144R	190	95
1 TrX	190	7 TrXHMLAHAE118C144R	190	95
1 TrX	190	8 TrXH11DMLAHAE144R161R	190	94
1 TrX	190	9 TrXH11DMLAHAE116G144R161R	190	94
1 TrX	190	10 TrXH11DMLAHAE118C144R161R	190	94
1 TrX	190	11 TrXH11DMLAHAE116G118C144R161R	190	93
2 TrX116G	190	3 TrX118C	190	98
2 TrX116G	190	4 TrXHMLAHAE144R	190	95
2 TrX116G	190	5 TrXHMLAHAE144R161R	190	94
2 TrX116G	190	6 TrXHMLAHAE116G144R	190	95
2 TrX116G	190	7 TrXHMLAHAE118C144R	190	94
2 TrX116G	190	8 TrXH11DMLAHAE144R161R	190	94
2 TrX116G	190	9 TrXH11DMLAHAE116G144R161R	190	94
2 TrX116G	190	10 TrXH11DMLAHAE118C144R161R	190	93
2 TrX116G	190	11 TrXH11DMLAHAE116G118C144R161R	190	94
3 TrX118C	190	4 TrXHMLAHAE144R	190	95
3 TrX118C	190	5 TrXHMLAHAE144R161R	190	94
3 TrX118C	190	6 TrXHMLAHAE116G144R	190	94
3 TrX118C	190	7 TrXHMLAHAE118C144R	190	95
3 TrX118C	190	8 TrXH11DMLAHAE144R161R	190	94
3 TrX118C	190	9 TrXH11DMLAHAE116G144R161R	190	93
3 TrX118C	190	10 TrXH11DMLAHAE118C144R161R	190	94
3 TrX118C	190	11 TrXH11DMLAHAE116G118C144R161R	190	94
4 TrXHMLAHAE144R	190	5 TrXHMLAHAE144R161R	190	99
4 TrXHMLAHAE144R	190	6 TrXHMLAHAE116G144R	190	99
4 TrXHMLAHAE144R	190	7 TrXHMLAHAE118C144R	190	99
4 TrXHMLAHAE144R	190	8 TrXH11DMLAHAE144R161R	190	98
4 TrXHMLAHAE144R	190	9 TrXH11DMLAHAE116G144R161R	190	98
4 TrXHMLAHAE144R	190	10 TrXH11DMLAHAE118C144R161R	190	98
4 TrXHMLAHAE144R	190	11 TrXH11DMLAHAE116G118C144R161R	190	97
5 TrXHMLAHAE144R161R	190	6 TrXHMLAHAE116G144R	190	98
5 TrXHMLAHAE144R161R	190	7 TrXHMLAHAE118C144R	190	98
5 TrXHMLAHAE144R161R	190	8 TrXH11DMLAHAE144R161R	190	99

Clustalw2--HTX18 pat seqa.txt						
5	TrXHMLAHAE144R161R	190	9	TrXH11DMLAHAE116G144R161R	190	98
5	TrXHMLAHAE144R161R	190	10	TrXH11DMLAHAE118C144R161R	190	98
5	TrXHMLAHAE144R161R	190	11	TrXH11DMLAHAE116G118C144R161R	190	98
6	TrXHMLAHAE116G144R	190	7	TrXHMLAHAE118C144R	190	98
6	TrXHMLAHAE116G144R	190	8	TrXH11DMLAHAE144R161R	190	98
6	TrXHMLAHAE116G144R	190	9	TrXH11DMLAHAE116G144R161R	190	98
6	TrXHMLAHAE116G144R	190	10	TrXH11DMLAHAE118C144R161R	190	97
6	TrXHMLAHAE116G144R	190	11	TrXH11DMLAHAE116G118C144R161R	190	98
7	TrXHMLAHAE118C144R	190	8	TrXH11DMLAHAE144R161R	190	98
7	TrXHMLAHAE118C144R	190	9	TrXH11DMLAHAE116G144R161R	190	97
7	TrXHMLAHAE118C144R	190	10	TrXH11DMLAHAE118C144R161R	190	98
7	TrXHMLAHAE118C144R	190	11	TrXH11DMLAHAE116G118C144R161R	190	98
8	TrXH11DMLAHAE144R161R	190	9	TrXH11DMLAHAE116G144R161R	190	99
8	TrXH11DMLAHAE144R161R	190	10	TrXH11DMLAHAE118C144R161R	190	99
8	TrXH11DMLAHAE144R161R	190	11	TrXH11DMLAHAE116G118C144R161R	190	98
9	TrXH11DMLAHAE116G144R161R	190	10	TrXH11DMLAHAE118C144R161R	190	98
9	TrXH11DMLAHAE116G144R161R	190	11	TrXH11DMLAHAE116G118C144R161R	190	99
10	TrXH11DMLAHAE118C144R161R	190	11	TrXH11DMLAHAE116G118C144R161R	190	99

NOTE: Some scores may be missing from the above table if the alignment was done using multiple CPU mode. Please check the output.

Alignment	Score	Sequence	Number	Sequence	Name	Sequence
CLUSTAL 2.0.5 multiple sequence alignment						
TrXHMLAHAE144R	50	QTIQPGTG	YHNGYFY	SYWNDGHGGV	TMTLPGGQ	QFSVNWSNSGNFVGGKG
TrXHMLAHAE116G144R	50	QTIQPGTG	YHNGYFY	SYWNDGHGGV	TMTLPGGQ	QFSVNWSNSGNFVGGKG
TrXH11DMLAHAE116G144R161R	50	QTIQPGTG	YHNGYFY	SYWNDGHGGV	TMTLPGGQ	QFSVNWSNSGNFVGGKG
TrXH11DMLAHAE116G118C144R161R	50	QTIQPGTG	YHNGYFY	SYWNDGHGGV	TMTLPGGQ	QFSVNWSNSGNFVGGKG
TrXH11DMLAHAE118C144R161R	50	QTIQPGTG	YHNGYFY	SYWNDGHGGV	TMTLPGGQ	QFSVNWSNSGNFVGGKG
TrXH11DMLAHAE144R161R	50	QTIQPGTG	YHNGYFY	SYWNDGHGGV	TMTLPGGQ	QFSVNWSNSGNFVGGKG
TrXHMLAHAE144R161R	50	QTIQPGTG	YHNGYFY	SYWNDGHGGV	TMTLPGGQ	QFSVNWSNSGNFVGGKG
TrXHMLAHAE118C144R	50	QTIQPGTG	YHNGYFY	SYWNDGHGGV	TMTLPGGQ	QFSVNWSNSGNFVGGKG
TrX	50	QTIQPGTG	YHNGYFY	SYWNDGHGGV	TMTLPGGQ	QFSVNWSNSGNFVGGKG
TrX116G	50	QTIQPGTG	YHNGYFY	SYWNDGHGGV	TMTLPGGQ	QFSVNWSNSGNFVGGKG
TrX118C	50	QTIQPGTG	YHNGYFY	SYWNDGHGGV	TMTLPGGQ	QFSVNWSNSGNFVGGKG
*****:***** * *****						
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TrXHMLAHAE116G144R	100	WQPGTKNK	VINFSGSY	NPNGNSYL	AVYGWSRN	PLIEYYIVENFGTYNPST
TrXH11DMLAHAE116G144R161R	100	WQPGTKNK	VINFSGSY	NPNGNSYL	AVYGWSRN	PLIEYYIVENFGTYNPST
TrXH11DMLAHAE116G118C144R161R	100	WQPGTKNK	VINFSGSY	NPNGNSYL	AVYGWSRN	PLIEYYIVENFGTYNPST
TrXH11DMLAHAE118C144R161R	100	WQPGTKNK	VINFSGSY	NPNGNSYL	AVYGWSRN	PLIEYYIVENFGTYNPST
TrXH11DMLAHAE144R161R	100	WQPGTKNK	VINFSGSY	NPNGNSYL	AVYGWSRN	PLIEYYIVENFGTYNPST
TrXHMLAHAE144R161R	100	WQPGTKNK	VINFSGSY	NPNGNSYL	AVYGWSRN	PLIEYYIVENFGTYNPST
TrXHMLAHAE118C144R	100	WQPGTKNK	VINFSGSY	NPNGNSYL	AVYGWSRN	PLIEYYIVENFGTYNPST
TrX	100	WQPGTKNK	VINFSGSY	NPNGNSYL	SVYGWSRN	PLIEYYIVENFGTYNPST
TrX116G	100	WQPGTKNK	VINFSGSY	NPNGNSYL	SVYGWSRN	PLIEYYIVENFGTYNPST
TrX118C	100	WQPGTKNK	VINFSGSY	NPNGNSYL	SVYGWSRN	PLIEYYIVENFGTYNPST
*****:***** * *****						
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TrXHMLAHAE116G144R	150	GATKHGEV	TSDGSVY	GIYRTQ	RVNAPSIE	GTATFYQYWSVRRNRSSGSV
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TrXH11DMLAHAE118C144R161R	150	GATKHGEV	TSDGSVY	DIYRTQ	RVNAPSIE	GTATFYQYWSVRRNRSSGSV
TrXH11DMLAHAE144R161R	150	GATKHGEV	TSDGSVY	DIYRTQ	RVNAPSIE	GTATFYQYWSVRRNRSSGSV
TrXHMLAHAE144R161R	150	GATKHGEV	TSDGSVY	DIYRTQ	RVNAPSIE	GTATFYQYWSVRRNRSSGSV
TrXHMLAHAE118C144R	150	GATKHGEV	TSDGSVY	DIYRTQ	RVNAPSIE	GTATFYQYWSVRRNRSSGSV
TrX	150	GATKLGEV	TSDGSVY	DIYRTQ	RVNQPSII	GTATFYQYWSVRRNRSSGSV
TrX116G	150	GATKLGEV	TSDGSVY	DIYRTQ	RVNQPSII	GTATFYQYWSVRRNRSSGSV
TrX118C	150	GATKLGEV	TSDGSVY	DIYRTQ	RVNQPSII	GTATFYQYWSVRRNRSSGSV
*****:***** * *****						
TrXHMLAHAE144R	190	NTANHFNA	WAQQLT	LGTM	DYQIVAVE	GYFSSGSASITVS
TrXHMLAHAE116G144R	190	NTANHFNA	WAQQLT	LGTM	DYQIVAVE	GYFSSGSASITVS
TrXH11DMLAHAE116G144R161R	190	NTANHFNA	WAQQLT	LGTM	DYQIVAVE	GYFSSGSASITVS
TrXH11DMLAHAE116G118C144R161R	190	NTANHFNA	WAQQLT	LGTM	DYQIVAVE	GYFSSGSASITVS
TrXH11DMLAHAE118C144R161R	190	NTANHFNA	WAQQLT	LGTM	DYQIVAVE	GYFSSGSASITVS
TrXH11DMLAHAE144R161R	190	NTANHFNA	WAQQLT	LGTM	DYQIVAVE	GYFSSGSASITVS

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                                Clustalw2--HTX18 pat seqa.txt
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TrXHMLAHAE118C144R            NTANHFNAWAQQGLTLGTMDYQIVAVEGYFSSGSASITVS 190
TrX                            NTANHFNAWAQQGLTLGTMDYQIVAVEGYFSSGSASITVS 190
TrX116G                        NTANHFNAWAQQGLTLGTMDYQIVAVEGYFSSGSASITVS 190
TrX118C                        NTANHFNAWAQQGLTLGTMDYQIVAVEGYFSSGSASITVS 190
                                *****

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PLEASE NOTE: Showing colors on large alignments is slow.

Guide Tree

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(
(
(
TrX:0.00175,
TrX116G:0.00351)
:0.00099,
TrX118C:0.00428)
:0.03914,
TrXHMLAHAE118C144R:0.00296)
:0.00181,
(
TrXHMLAHAE144R161R:0.00115,
(
TrXH11DMLAHAE144R161R:0.00184,
(
TrXH11DMLAHAE116G144R161R:0.00188,
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:0.00219,
TrXH11DMLAHAE118C144R161R:0.00307)
:0.00079)
:0.00411)
:0.00444)
:0.00016,
TrXHMLAHAE144R:0.00066,
TrXHMLAHAE116G144R:0.00461);

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Cladogram

Right-click on the above tree to see display options.
Problems printing? Read how to print a Phylogram or Cladogram.